D4 Fig. 7: Relationship between *refre*1 sequence (SEQ ID NO: 1) and primers (SEQ ID NOS: 5-34, respectively, in order of appearance).

Please amend page 6, line 19, to read as follows:

D5 Fig. 9: Total sequence of designed *refre*1 (SEQ ID NOS: 1 & 2).

Please amend page 24, lines 5-6, to read as follows:

D6 Hybrid primer (dT^{17} adapter primer):
5'-GACTCGAGTCGACATCGATTTTTTTTTTTTTTTT-3' (SEQ ID NO: 35)

Please amend page 24, lines 18-19, to read as follows:

D7 Primer specific to hybrid primer:
5'-GACTCGAGTCGACATCG-3' (SEQ ID NO: 3)

Please amend page 24, lines 20-21, to read as follows:

D8 5' primer of FRE1:
5'-ACACTTATTAGCACTTCATGTATT-3' (SEQ ID NO: 4)

IN THE CLAIMS:

Please cancel claims 30-45 without prejudice.

Kindly add the following new claims:

D9 46. A method of making a nucleic acid for modifying a base sequence of a gene for transforming a plant, comprising modifying the sequence of the gene in accordance with features (A) and (B) without altering the amino acid sequence thereof, for eliminating sequences relating to poly(A) addition,

wherein features (A) and (B) are defined as follows:

(A) GT rich regions comprising 8 or more consecutive bases of G or T within the